

59. (New) The method of claim 18, wherein said primers further comprise one or more hairpin structures.

60. (New) The method of claims 18 or 59, wherein said one or more primers further comprise a detectable label at or near their 3' and/or 5' termini.

61. (New) The method of claim 20, wherein said one or more oligonucleotides further comprise one or more detectable labels at or near their 3' and/or 5' termini.

62. (New) The method of claim 47, wherein said one or more oligonucleotides further comprise one or more detectable labels at or near their 3' and/or 5' termini.

91 63. (New) The method of any one of claims 10, 11, 12, 18, 20 or 47, wherein said detectable label is at the fourth base from the 3' termini.

64. (New) The method of any one of claims 10, 11, 12, 18, 20 or 47, wherein said detectable label is at the fifth base from the 3' termini.

65. (New) The method of any one of claims 10, 11, 12, 18, 20 or 47, wherein said detectable label is at the sixth base from the 3' termini.

66. (New) The method of any one of claims 10, 11, 12, 18, 20 or 47, wherein said detectable label is attached to one of the ten 3'-most terminal nucleotides.

67. (New) The method of any one of claims 10, 11, 12, 18, 20 or 47, wherein said detectable label is attached to one of the twenty 3'-most terminal nucleotides.

Please substitute the following claim 10 for the pending claim 10:

10. (Once amended) A method for the quantification or detection of one or more target nucleic acid molecules in a sample comprising hybridizing one or more detectably labeled oligonucleotides with one or more molecules to be detected or quantified, wherein said one or more oligonucleotides comprise one or more detectable labels located internally and said one or more labels undergo a detectable change in an observable property upon becoming part of a double stranded molecule, and detecting the presence or absence and/or quantifying the amount of said one or more target nucleic acid molecules.

~~Please substitute the following claim 11 for the pending claim 11:~~

11. (Once amended) A method for the quantitation or detection of one or more nucleic acid molecules in a sample during nucleic acid synthesis comprising:

mixing one or more nucleic acid templates with one or more oligonucleotides, wherein said one or more oligonucleotides comprise one or more detectable labels located internally and said one or more labels undergo a detectable change in an observable property upon becoming part of a double stranded molecule;

incubating said mixture under conditions sufficient to synthesize one or more nucleic acid molecules complementary to all or a portion of said one or more templates, said one or more synthesized nucleic acid molecules comprising said one or more oligonucleotides; and detecting the presence or absence or quantifying the amount of said one or more

synthesized nucleic acid molecules by measuring said one or more detectable labels.

~~Please substitute the following claim 12 for the pending claim 12:~~

12. (Once amended) A method for quantitation or detection of one or more nucleic acid molecules in a sample during nucleic acid amplification comprising:

mixing one or more nucleic acid templates with one or more oligonucleotides under conditions sufficient to amplify one or more nucleic acid molecules complementary to all or a portion of said one or more templates, said one or more amplified nucleic acid molecules comprising said one or more oligonucleotides, wherein said one or more oligonucleotides comprise one or more detectable labels located internally and said one or more labels undergo a detectable change in an observable property upon becoming part of a double stranded molecule; and

detecting the presence or absence or quantifying the amount of said one or more nucleic acid molecules by measuring the detectable labels of said oligonucleotides.

~~Please substitute the following claim 18 for the pending claim 18:~~

18. (Once amended) A method for amplifying a double stranded nucleic acid molecule, comprising:

providing a first and second primer, wherein said first primer is complementary to a sequence within or at or near the 3'-termini of the first strand of said nucleic molecule and said second primer is complementary to a sequence within or at or near the 3'-termini of the second strand of said nucleic acid molecule;

hybridizing said first primer to said first strand and said second primer to said second

SUB  
CA  
COO<sup>+</sup>

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strand in the presence of one or more polymerases, under conditions such that a third nucleic acid molecule complementary to all or a portion of said first strand and a fourth nucleic acid molecule complementary to all or a portion said second strand are synthesized;

denaturing said first and third strands, and said second and fourth strands; and

repeating the above steps one or more times, wherein one or more of the primers comprise a detectable label located internally.

Please substitute the following claim 20 for the pending claim 20:

SUB  
CB

CF

20. (Once amended) A method for the quantification or detection of nucleic acid molecules comprising:

mixing one or more labeled oligonucleotides with one or more nucleic acid molecules to be detected or quantitated, wherein said one or more oligonucleotides comprise one or more detectable labels located internally; and

detecting or measuring an increase in fluorescence associated with said one or more oligonucleotides hybridizing to said one or more nucleic acid molecules.

Please substitute the following claim 47 for the pending claim 47:

SUB  
C4

C5

47. (Once amended) A method for detecting a target nucleic acid sequence, comprising:

contacting a sample containing a mixture of nucleic acid molecules with at least one oligonucleotide capable of hybridizing with a target nucleic acid molecule and comprising a detectable moiety located internally, wherein the detectable moiety undergoes a change

SUB  
C4  
COO4.

AS10K

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in one or more observable properties upon hybridization to the target nucleic acid molecule;

and

observing the observable property, wherein a change in the observable property  
indicates the presence of the target nucleic acid sequence.

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